

JC07 Rec'd PCT/PTO 16 JAN 20

SEQUENCE LISTING

GENERAL INFORMATION:

(i) APPLICANT: PLANTECHNO S.R.L.

(ii) TITLE OF INVENTION:

SYNTHETIC POLYNUCLEOTIDE ENCODING HUMAN LACTOFERRIN,
VECTORS, CELLS AND TRANSGENIC PLANTS CONTAINING IT

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Società Italiana Brevetti

(B) STREET: Piazza di Pietra, 39

(C) CITY: Roma

(D) COUNTRY: Italy

(E) POSTAL CODE: I-00186

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS Rev. 5.0

(D) SOFTWARE: Microsoft Word 6.0

(viii) ATTORNEY INFORMATION

(A) NAME: LEONE, Mario (Eng.)

(B) REFERENCE: PC-EBR

(ix) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: 06/695441

(B) TELEFAX: 06/69544830

(C) TELEX: 612287 ROPAT

T02220-EBR460

(1) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 2079 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURES

(A) NAME: LFUSYN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGC CGT AGG AGA AGG AGT GTT CAA TGG TGC GCA GTA TCA CAA CCA 45
G R R R R S V Q W C A V S Q P

GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTT 90
E A T K C F Q W Q R N M R K V

CGT GGA CCT CCT GTA TCT TGC ATA AAG AGA GAT TCA CCC ATC CAG 135
R G P P V S C I K R D S P I Q

TGT ATC CAG GCA ATT GCG GAA AAC AGA GCT GAT GCT GTG ACT CTT 180
C I Q A I A E N R A D A V T L

GAT GGT GGT TTC ATA TAC GAG GCA GGA CTT GCC CCA TAC AAA CTG 225
D G G F I Y E A G L A P Y K L

CGA CCT GTA GCG GCG GAA GTC TAC GGG ACC GAA AGA CAA CCA CGA 270
R P V A A E V Y G T E R Q P R

ACT CAC TAT TAT GCT GTG GCT GTT GTG AAG AAG GGC GGA TCT TTT 315
T H Y Y A V A V V K K G G S F

CAG CTG AAC GAA CTT CAA GGT CTG AAG TCA TGC CAC ACA GGA CTT 360
Q L N E L Q G L K S C H T G L

CGC AGG ACC GCT GGA TGG AAT GTC CCT ATA GGG ACA CTT CGT CCA 405
R R T A G W N V P I G T L R P

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TTC TTG AAT TGG ACG GGT CCA CCT GAG CCC ATT GAG GCA GCT GTG 450
F L N W T G P P E P I E A A V

GCA AGA TTC TTC TCA GCC TCT TGT GTT CCA GGT GCA GAT AAA GGA 495
A R F F S A S C V P G A D K G

CAA TTC CCC AAC CTT TGT CGC CTG TGT GCG GGG ACA GGG GAA AAC 540
Q F P N L C R L C A G T G E N

AAA TGT GCA TTC TCA TCC CAG GAA CCG TAC TTC AGC TAC TCT GGT 585
K C A F S S Q E P Y F S Y S G

GCC TTT AAG TGT CTT AGA GAC GGT GCT GGA GAT GTT GCT TTT ATT 630
A F K C L R D G A G D V A F I

AGA GAG AGC ACA GTG TTT GAG GAT CTT TCA GAC GAG GCT GAA AGG 675
R E S T V F E D L S D E A E R

GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGT AAG CCA GTT 720
D E Y E L L C P D N T R K P V

GAC AAG TTC AAA GAT TGC CAT CTT GCA CGG GTC CCT TCT CAT GCC 765
D K F K D C H L A R V P S H A

GTT GTG GCA CGA AGT GTT AAT GGA AAG GAG GAT GCC ATC TGG AAT 810
V V A R S V N G K E D A I W N

CTT CTC CGC CAA GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG 855
L L R Q A Q E K F G K D K S P

AAA TTC CAG CTC TTT GGT TCC CCT AGT GGG CAG AAA GAT CTT CTG 900
K F Q L F G S P S G Q K D L L

TTC AAG GAC TCT GCC ATT GGG TTT TCG AGA GTG CCA CCT AGG ATA 945
F K D S A I G F S R V P P R I

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GAT TCT GGG TTG TAC CTT GGC TCC GGA TAC TTT ACT GCA ATT CAG 990
D S G L Y L G S G Y F T A I Q

AAC TTG AGG AAA AGT GAG GAG GAA GTT GCT GCC CGG CGT GCG CGG 1035
N L R K S E E E V A A R R A R

GTC GTT TGG TGT GCG GTG GGA GAG CAA GAG TTG CGC AAG TGT AAC 1080
V V W C A V G E Q E L R K C N

CAG TGG AGT GGT TTG AGC GAA GGA TCT GTG ACC TGC TCA TCG GCC 1125
Q W S G L S E G S V T C S S A

TCC ACT ACA GAA GAT TGC ATC GCC CTG GTG TTG AAA GGA GAA GCT 1170
S T T E D C I A L V L K G E A

GAT GCC ATG AGT TTG GAT GGA GGA TAT GTT TAC ACT GCA GGT AAA 1215
D A M S L D G G Y V Y T A G K

TGT GGT TTG GTG CCT GTC CTT GCA GAG AAC TAC AAA TCA CAA CAA 1260
C G L V P V L A E N Y K S Q Q

AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT AGA CCT GTG GAA GGA 1305
S S D P D P N C V D R P V E G

TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC ACT AGC CTT ACC 1350
Y L A V A V V R R S D T S L T

TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC GCC GTG GAC 1395
W N S V K G K K S C H T A V O

AGG ACT GCA GGT TGG AAT ATC CCC ATG GGA TTG CTC TTC AAC CAG 1440
R T A G W N I P M G L L F N Q

ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT GCC 1485
T G S C K F D E Y F S Q S C A

CCT GGT TCT GAC CCA AGA TCT AAT CTC TGT GCT TTG TGT ATT GGA 1530

T02280-2282460

P	G	S	D	P	R	S	N	L	C	A	L	C	I	G		
GAT	GAG	CAA	GGT	GAG	AAT	AAG	TGC	GTT	CCC	AAC	AGC	AAC	GAG	AGA	1575	
D	E	Q	G	E	N	K	C	V	P	N	S	N	E	R		
TAC	TAC	GGT	TAC	ACT	GGG	GCT	TTC	CGT	TGC	TTG	GCT	GAG	AAT	GCT	1620	
Y	Y	G	Y	T	G	A	F	R	C	L	A	E	N	A		
GGA	GAC	GTT	GCA	TTT	GTG	AAA	GAT	GTC	ACT	GTC	TTG	CAG	AAC	ACT	1665	
G	D	V	A	F	V	K	D	V	T	V	L	Q	N	T		
GAT	GGA	AAT	AAC	AAT	GAG	GCA	TGG	GCT	AAG	GAT	TTG	AAG	CTT	GCA	1710	
D	G	N	N	N	E	A	W	A	K	D	L	K	L	A		
GAC	TTT	GCG	TTG	CTG	TGC	CTC	GAT	GGC	AAA	CGT	AAG	CCT	GTG	ACT	1755	
D	F	A	L	L	C	L	D	G	K	R	K	P	V	T		
GAA	GCT	AGA	AGC	TGC	CAT	CTT	GCC	ATG	GCC	CCG	AAT	CAT	GCT	GTG	1800	
E	A	R	S	C	H	L	A	M	A	P	N	H	A	V		
GTG	TCT	CGT	ATG	GAT	AAG	GTG	GAA	CGC	TTG	AAA	CAG	GTG	TTG	CTC	1845	
V	S	R	M	D	K	V	E	R	L	K	Q	V	L	L		
CAC	CAA	CAG	GCT	AAA	TTT	GGT	AGA	AAT	GGA	TCT	GAC	TGC	CCG	GAC	1890	
H	Q	Q	A	K	F	G	R	N	G	S	D	C	P	D		
AAG	TTT	TGC	TTA	TTC	CAG	TCT	GAA	ACC	AAA	AAC	CTT	TTG	TTC	AAT	1935	
K	F	C	L	F	Q	S	E	T	K	N	L	L	F	N		
GAC	AAC	ACT	GAG	TGT	CTT	GCC	AGA	CTC	CAT	GGC	AAA	ACA	ACA	TAT	1980	
D	N	T	E	C	L	A	R	L	H	G	K	T	T	Y		
GAA	AAA	TAT	TTG	GGA	CCA	CAG	TAT	GTC	GCA	GGC	ATT	ACT	AAT	CTG	2025	
E	K	Y	L	G	P	Q	Y	V	A	G	I	T	N	L		
AAA	AAG	TGC	TCA	ACC	TCC	CCA	CTC	CTA	GAA	GCC	TGT	GAA	TTC	CTA	2070	
K	K	C	S	T	S	P	L	L	E	A	C	E	F	L		

AGG AAG TAA

2079

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 30 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGATCCATGG GCCGTAGGAG AAGGAGTGTT

30

(3) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 32 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAGCTCCTTC GGTTTTACTT CCTGAGGAAT TC

32

(4) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 42 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

T02280*E2BET460

(A) NAME: PLT 48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCTAGATAAA ATAATCTATA CATTAAAAAA TTTGATTTTA AA 42

(5) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 36 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

(A) NAME: PLT 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGATCCGACT GAGTCGGATA AGAAGAAAAG AAAAGA 36

(6) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 36 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

(A) NAME: PLT 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCTAGAGTTT TCAAATTGGA ATTTTAATGT GTGTTG 36

(7) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 36 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: oligonucleotide
(ix) FEATURES
(A) NAME: PLT 51
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCCACC TTAAGGAGGT TGCAACGAGC GTGGCA 36

- (8) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 250 bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: oligonucleotide
(ix) FEATURES
(A) NAME: PLT 120
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGC CGT AGG AGA AGG AGT GTT CAA TGG TGC GCA GTA TCA CAA CCA GAG
GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTT CGT GGA
CCT CCT GTA TCT TGC ATA AAG AGA GAT TCA CCC ATC CAG TGT ATC CAG
GCA ATT GCG GAA AAC AGA GCT GAT GCT GTG ACT CTT GAT GGT GGT TTC
ATA TAC GAG GCA GGA CTT GCC CCA TAC AAA CTG CGA CCT GTA GCG GCG
GAA GTC TAC G

- (9) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 250 bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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F02280-22824260

- (ii) MOLECULE TYPE: oligonucleotide
(ix) FEATURES
 (A) NAME: PLT 121
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GC ACC TGG AAC ACA AGA GGC TGA GAA GAA TCT TGC CAC AGC TGC CTC
AAT GGG CTC AGG TGG ACC CGT CCA ATT CAA GAA TGG ACG AAG TGT CCC
TAT AGG GAC ATT CCA TCC AGC GGT OCT GCG AAG TCC TGT GTG GCA TGA
CTT CAG ACC TTG AAG TTC GTT CAG CTG AAA AGA TCC GCC CTT CTT CAC
AAC AGC CAC AGC ATA ATA GTG AGT TCG TGG TTG TCT TTC GGT CCC GTA
GAC TTC CGC CG

- (10) INFORMATION FOR SEQ ID NO:10:
(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 250 bp
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: oligonucleotide
(ix) FEATURES
 (A) NAME: PLT 122
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAC TGG CTT ACG AGT GTT GTC TGG GCA GAG TAA CTC ATA CTC GTC
CCT TTC AGC CTC GTC TGA AAG ATC CTC AAA CAC TGT GCT CTC TCT
AAT AAA AGC AAC ATC TCC AGC ACC GTC TCT AAG ACA CTT AAA GGC
ACC AGA GTA GCT GAA GTA CGG TTC CTG GGA TGA GAA TGC ACA TTT
GTT TTC CCC TGT CCC CGC ACA CAG GCG ACA AAG GTT GGG GAA TTG

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T00230-E286460

TCC TTT ATC TGC ACC TGG AAC ACA A

(11) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 255 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTA CAA CCC AGA ATC TAT CCT AGG TGG CAC TCT CGA AAA CCC AAT GGC

AGA GTC CTT GAA CAG AAG ATC TTT CTG CCC ACT AGG GGA ACC AAA GAG

CTG GAA TTT CGG TGA CTT GTC CTT TCC AAA CTT TTC CTG TGC TTG GCG

GAG AAG ATT CCA GAT GGC ATC CTC CTT TCC ATT AAC ACT TCG TGC CAC

AAC GGC ATG AGA AGG GAC CCG TGC AAG ATG GCA ATC TTT GAA CTT GTC

AAC TGG CTT ACG AGT

(12) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 251 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

09743823.108201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGATGAGAG	CGCGGTTCCC	ATTACTGTTG	CTGGGAGTTG	TTTTCTAGC	50
ATCAGTTTCT	GTCTCATTTG	GCATTGCGTA	TTGGGAAAAG	CAGAACCCCA	100
GTCACAACAA	GTGCCTCCGA	AGTTGCAATA	GCGAGAAAGA	CTCCTACAGG	150
AACCAAGCAT	GCCACGCTCG	TTGCAACCTC	CTTAAGGTG		189

(15) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 250 bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGCAATCCC	ATGGGGATAT	TCCAACCTGC	AGTCCTGTCC	ACGGCGGTGT	50
GGCAGGACTT	CTTGCCTTTC	ACAGAGTTCC	AGGTAAGGCT	AGTGTCTGAT	100
CTCCTAACCA	CCGCCACAGC	AAGATATCCT	TCCACAGGTC	TATCCACACA	150
GTTAGGATCA	GGGTCACTGC	TTTGTGTGTA	TTTGTAGTTC	TCTGCAAGAC	200
AGGCACCAAA	CCACATTTAC	CTGCAGTGTA	AACATATCCT	CCATCCAAAC	250

(16) INFORMATION FOR SEO ID NO:16:

(1) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 254 bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCATCAGTGT	TCTGCAAGAC	AGTGACATCT	TTCACAAATG	CAACGTCTCC	50
AGCATTCTCA	GCCAAGCAAC	GGAAAGCCCC	AGTGTAACCG	TAGTATCTCT	100
CGTTGCTGTT	GGGAACGCAC	TTATTCTCAC	CTTGCTCATC	TCCAATACAC	150
AAAGCACAGA	GATTAGATCT	TGGGTCAGAA	CCAGGGGCAC	AGCTTTGACT	200
GAAATATTCA	TCAAATTTGC	AGGAGCCCGT	CTGGTTGAAG	AGCAAGCCCA	250
TGGG					254

(17) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 229 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAGTCAGAT CCATTTCTAC CAAATTTAGC CTGTTGGTGG AGCAACACCT 50
GTTTCAAGCG TTCCACCTTA TCCATACGAG ACACCACAGC ATGATTCGGG 100
GCCATGGCAA GATGGCAGCT TCTAGCTTCA GTCACAGGCT TACGTTTGCC 150
ATCGAGGCAC AGCAACGCAA AGTCTGCAAG CTTCAAATCC TTAGCCCATG 200
CCTCATTGTT ATTCCATCA GTGTTCTGC 229

(18) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 210 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

- (A) NAME: PLT 128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTACTTCCTT AGGAATTCAC AGGCTTCTAG GAGTGGGGAG GTTGAGCACT 50
TTTTCAGATT AGTAATGCCT GCGACATACT GTGGTCCCAA ATATTTTCA 100
TATGTTGTTT TGCCATGGAG TCTGGCAAGA CACTCAGTGT TGTCATTGAA 150
CAAAAGGTTT TTGGTTTCAG ACTGGAATAA GCAAACTTG TCCGGGCAGT 200
CAGATCCATT 210

(19) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 30 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

10074322-00001

(ix) FEATURES

(A) NAME: PLT 129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCATGG GCCGTAGGAG AAGGAGTGT

30

(20) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 28 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURES

(A) NAME: PLT 120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAGCTCTTAC TTCCTTAGGA ATTCACAG

28

(21) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURES

(D) OTHER INFORMATION: sequence of promoter of gene encoding 7S basic globulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TAAAATAATC TATACATTAA AAAATTTGAT TTTAAAATTT TAGAAATTCA	50
TGATTTTATT TTTTTTTACC AGAAATCCGT TAATATTGTT AAAATATTAC	100
CAACTAATTT ATAAATTTTA TTTTAAGGCA ATTAAGCATG TTTGATAAAA	150
TATATATATT GTTATAAATA CTTTTCAAAA GTATAAAGTT GATGATGGCG	200
TGGTGGTAGA TTATTTTAGT TCTAGGTTCTG AATGCAAGTT GGTTTAGACA	250
TTTAGCCTTA TTCTTTTTTC TAACCAAAAT AAATGTAAAT GGAAACCTT	300
TAGGAAAAAA AAGAAATCAA AATTGAAAAC ATCATCCGGT GGAGTCGAGA	350
AGCCACACC CACGTGACCC AACAATATTA AAATAAGAGT TTGCTCTACA	400

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(22) INFORMATION FOR SEO ID NO:22:

(A) LENGTH: bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix) FEATURES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTTTTCAAAT	TTGAATTTTA	ATGTGTGTTG	TAAGTATAAA	TTTAAAATAA	50
AAATAAAAAC	AATTATTATA	TCAAAATGGC	AAAAACATTT	AATACGTATT	100
ATTTATTAAA	AAAATATGTA	ATAATATATT	TATATTTTAA	TATCTATTCT	150
TATGTATTTT	TTAAAAATCT	ATTATATATT	GATCAACTAA	AATATTTTTA	200
TATCTACACT	TATTTTGCAT	TTTTATCAAT	TTTCTTGCGT	TTTTTGGCAT	250

